

PATENT APPLICATION
BRASSICA POLYMORPHISMS

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PATENT

Attorney Docket No. 16528X-030100US

BRASSICA POLYMORPHISMS

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CROSS-REFERENCE TO RELATED APPLICATION

The present application derives priority from provisional application 60/032,069, filed December 2, 1996, which is incorporated by reference in its entirety for all purposes.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) means a variation in DNA sequence that alters the length of a

restriction fragment as described in Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment. RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein. Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective or variant protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects. Single nucleotide polymorphisms can be used in the same manner as RFLPs, and VNTRs but offer several advantages. Single nucleotide polymorphisms occur with greater frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. Also, the different forms of

characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Despite the increased amount of nucleotide sequence data being generated in recent years, only a minute proportion of the total repository of polymorphisms has so far been identified. The paucity of polymorphisms hitherto identified is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of oligonucleotides in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of subjects.

SUMMARY OF THE INVENTION

The invention provides nucleic acid segments containing at least 10, 15 or 20 contiguous bases from a fragment shown in Table 1 including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Some segments are 10-20 or 10-50 bases long. Preferred segments include a diallelic polymorphic site.

The invention further provides allele-specific oligonucleotides that hybridizes to a segment of a fragment shown in Table 1 or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence of Table 1 or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in Table 1.

The invention further provides a method of analyzing a nucleic acid from a subject. The method determines which base or bases is/are present at any one of the polymorphic sites shown in Table 1. Optionally, a set of bases occupying a set

of the polymorphic sites shown in Table 1 is determined. This type of analysis can be performed on a plurality of subjects who are tested for the presence of a phenotype. The presence or absence of phenotype can then be correlated with a base or set of bases present at the polymorphic sites in the subjects tested.

BRIEF DESCRIPTION OF THE FIGURE

Fig. 1 shows probe arrays tiles for two allelic forms of the Brassira 18A2 polymorphism.

DEFINITIONS

A nucleic acid, such an oligonucleotide, oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. Preferred nucleic acids of the invention include segments of DNA, or their complements including any one of the polymorphic sites shown in Table 1. The segments are usually between 5 and 100 bases, and often between 5-10, 5-20, 10-20, 10-50, 20-50 or 20-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in Table 1. Methods of synthesizing oligonucleotides are found in, for example, *Oligonucleotide Synthesis: A Practical Approach* (Gait, ed., IRL Press, Oxford, 1984).

Hybridization probes are oligonucleotides capable of binding in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

The term primer refers to a single-stranded oligonucleotide capable of acting as a point of initiation of template-directed DNA synthesis under appropriate conditions (i.e., in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer but

typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template but must be sufficiently complementary to hybridize with a template. The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair means a set of primers including a 5' upstream primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3', downstream primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

Linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome, and can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

Polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as a the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two forms. A triallelic polymorphism has three forms.

A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is

usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridizations.

Nucleic acids of the invention are often in isolated form. An isolated nucleic acid means an object species that is the predominant species present (i.e., on a molar basis it is more abundant than any other individual species in the composition). Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods).

DESCRIPTION OF THE PRESENT INVENTION

I. Novel Polymorphisms of the Invention

The present application provides oligonucleotides containing polymorphic sequences isolated from two *Brassica* species, *B. napus* and *B. oleracea*. The invention also includes various methods for using those novel oligonucleotides to identify, distinguish, and determine the relatedness of individual strains or pools of nucleic acids from plants within the family *Cruciferae*.

The genus *Brassica* is part of the family *Cruciferae*. Members of the *Brassica* genus have been described as Old World Temperate Zone herbs of the mustard family with beaked cylindrical pods. Merriam-Webster's Collegiate Dictionary, Tenth ed., p.139 (1993). Many cruciferous plants are important agricultural items and include many foodstuffs (condiments, oilseeds, and vegetables). For example, canola (a type of *Brassica napus*) is one of the largest crops in Canada.

The sequences in Table 1 were isolated from *B. napus* and *B. oleracea* using oligonucleotide primers designed from expressed DNA sequences from *Arabidopsis thaliana*, a relative of *Brassica napus* and member of the *Cruciferae* family. See Hofte et al., An inventory of expressed sequence tags obtained by partial sequencing of cDNAs from *Arabidopsis thaliana*, *Plant J.*, Vol.4, pp. 1051-1061 (1993) and Newman et al., Genes Galore: A Summary of Methods for Accessing Results from Large-Scale Partial Sequencing of Anonymous *Arabidopsis* cDNA Clones, *Plant Physiol.*, Vol. 106, pp. 1241-1255 (1994). There is a high degree of homology between the coding sequences of *Arabidopsis*, *Brassica*, and other members of the *Cruciferae* family.

The designations in Table 1 are as follows. The first number, preceding the "-" is an arbitrarily assigned identification number for a polymorphism. The first number after the "-" is the *Brassica* strain name corresponding to the upper allele sequence. The next number designates the primer pair used for the PCR amplification. The sequences of primers are described at the web site (http://www.yorku.ca/ftp/york_other/cgat/) (incorporated by reference in its entirety for all purposes). The last number is the name of the strain for the lower allele sequence. For example 1-85/5B5/86-1 means that polymorphic site 1 was identified by comparing strains 85 and 86-1 at a segment amplified by primers 5B5. Each sequence in the table includes a polymorphic site shown in square brackets [] and flanking bases common to both strains being compared. The upper and lower sequences in the square brackets are from the two

strains being compared (upper strand corresponding to the first designated strain). A "/" within square brackets followed or preceded by a blank space represents an addition/deletion polymorphism. Sequences having marker names with a single / (such as 24-10C8/N2), indicate a polymorphic position but do not show comparisons with a second strand. An asterisk indicates triallelic markers. The designation N in Table 1 indicates a base whose identity was not determined.

TABLE 1

MARKER NAME SEQUENCE

1-85/5B5/86-1	AGCAAGCTTACATGCGTGGA[GT/AA]GAGAGTCCTCGAGATCAACC
2-85/5B12/N3-1	CCTTGATCTCTCAAGTAATC[A/G]TCTCACCGBAAGATCCCTGA
3-85/5C3/86-2	ACCATCCATTAAACTGTATC[A/G]TCGCAATCTAACCCAAAGTT
4-85/5E1/86-1	TAAAGCAAAGAGAGTCTTAC[C/A]GTCTGCTGCATGATATACCC
5-85/5E1/86-2	CTACTGATAGTGAACCAACC[C/A]ATCCCCAAATTTAAAGCAA
6-85/6A11/86	ATCCTATTGGTAGTAACACA[G/A]ATTGAGTTAATGTTGCAGGG
7-N1/6A11/N2	AGGCAAAGCGGTAGTTGCAA[G/A]ACTGCTTCTCACGAGGTAAT
8-N1/6A9/N2-1	CCAGCTTCAATGTCTGCATG[C/A]TTGTGTCGATGCCAAAGTTC
9-N1/6A9/N2-2	AAAGTTTCATTACGATGATCT[A/G]ACCCGTCAGTCATCCATGGA
10-85/6A12/86	CTTCCCCCCTCAATACCTC[T/G]TTCAAAAGTGAAAGTGCAG
11-N1/6D1/N2-1	ATTTTGTTTTGTCTTCTTGTC[G/C]GGTCAGGTGAGAACAAGTT
12-N1/6H5/N2	AAACCAGAGCCACCTCCTTA[C/]CCACCTCATCGTTTCCTTTC
13-86/6F11/N2-2	GATTTGACCGCAGTCTCAC[G/T]GAGGATGAGTATATCGCTTT
14-N1/6F11/N2	TAGGACAGGCAAACAATCTA[C/A]GCGGTCAAAATCCGATTTG
16-N1/8B5/N2	ACTCAAAAAACGATACCTC[G/C]GCCGTCCTCGCCGTCTCGC
17-N1/8D4/N2-1	CAGGAGACAGTTACAGTCCC[/A]CAGAGTCGAAGGATCTCGAA
18-85/8D4/86-2	CTGATCTTGAAGGAGAGACC[A/G]CCACAAGGTTCCATCCTATG
19-85/8H11/86	AGTGCGAGGCTCAGTTGGAT[G/T]ATTAGGTTGTCAGTAAATCA
20-85/10B8/86	NAGGTCCATGATGATGACAA[T/A]AAAGGTATTCCACATGTCAA
21-N2/10B8/N3-2	ACATCCAACTTTTCTCCAGT[T/C]CTTTATTCTATCCTGATTG
22-N2/10B8/N3-1	AAGGTATTCCATTGGTATAC[A/C]TCCAACTTTTCTCCAGTTCT
23-85/10B9/86	GACCTTCTTGGGAAAGAAAG[T/C]TGTAACCGCGTCGAGATTG
24-10C8/N2	ATAGAAACCGCCGATGCTCA[A]GGACACGCCACCGTCTTCGT
25-10C8/N2	CACCTTTCTTCGTGGCTAAAT[T]CTTCGCCCGAGCCGGTCTCA
26-10D2/N1	GTTATCATCAGTACCGGTAT[T]AACCCCAAGGCTAATTCCTTA
27-85/10D2	TTGGGTATCTACGGAAGTAT[C]ATCGCTGTTATCATCAGTAC
28-N1/10E12/N2-1	GGAATTCAATACTCGCCAAC[G/T]TCTTCATGCTGTCGTCGGC

29-N1/10E12/N2-2 TCCTTACGCTTCAAGCGCA [C/G] CGGCTGGCTCATGGGTGTCC
 30-N1/10F4/N2 TGTATCTATGCGGTGGCTGC [G/C] GTCTCCGTTCCGCCAGTAC
 31-10F4/N2 GCGCCAGTACCGCCGGTTAC [A] ATCTcACTGCCTTCAAGTCC
 32-85/10F4/N2 GCGCCAGTACCGCCGGTTAC [G/A] ATCTTAAATGCCTTCAAGTTC
 5 33-85/10F9/N1-2 AACTTGAATTCCACAACIT [G/C] AGAAACTTCGATGTGGTGCC
 34-85/10F9/86 CGGTACTGCGAAAGCTGGAG [C/G] ATCAACTTGGAAATCCACAA
 35-86/10F12 AAAAGTGCTATTGTTAGGT [G] GATGCTGCTCCGTTCAAGCA
 36-85/10H6/86 GTCAAAAGCCACGGATTCAA [G/A] AACGTGCTCTTCTTGCGCCT
 38-85/10F12/86 AAACCAGGGTCTTGTATGTG [T/] GTCTACAAGCTTCCAACAA
 10 39-85/11B7/86 AANACCCTGAGCTCATGCCT [C/T] TGACCCATGTTCTTGCCACC
 40-85/11C4/86 TTTGGGACCGTTGGAGTTGC [A/G] TCTGCGGTATGACGGTGA
 41-85/11D4/86-2 AATCTTTGCCATTGCTGTCA [A/G] TATCTTCGTAGCTTACGCT
 43-N2/11D11/N3 GACAACGCTGGTGGTATTGC [C/T] GAAATGGCTGGAATGAGCCA
 15 44-86/11D11/N3 GCTGCTCTAGGGATGCTCAG [C/T] ACCATCGCCACCGGTTTGGC
 45-85/11D11/86 ATGCTCAGCACCATCGCCAC [T/C] GGGTTgGCGATTGATGCTTA
 46-N2/11E3/N8a GAGAAAGTGCTTGTGGAGAT [C/T] TACAAGTCCATACTGATGGC
 47-86/11E3/N2a AATGCTTGTGGAGATTACA [G/A] GTCCATACTGATGGCGCAGG
 48-86/11E3/N2b AATGCTTGTGGAGATcTACA [G/A] GTCCATACTGATGGCGCAGG
 20 49-85/11F12/86 AATGATTGGTTTGAAGCA [T/A] ACAGCTGGTACGCTTGATAT
 50-85/11F7/86 GATAGGGCGAAGAGAGGGAA [G/A] AGTCTTGAGAGGAAAGAGAT
 CTCTCTCTCCACAAAGACAC [A/C] GCTTTCTCCATGACCTTCGG
 52-85/11H5/86-2 TCTCTGACGTCATGAAAGCT [C/A] ATGGCAAAATTGCTGATGGA
 53-85/11H6/86-1a GTTATCGATCGCGTGGTCCG [T/C] GAAACCCAAAATaCACCTTT
 25 54-85/11H6/86-1b GTTATCGATCGCGTGGTCCG [T/C] GAAACCCAAAATtCACCTTT
 55-85/12B6/N3 CGTCAGCCTTCTTCCGCCGC [A/C] GTCGTCTCCGCAACCGTGC
 56-86/12B6/85a TGTCTCTTCCGTCAGCCTTC [C/T] TCCGCCGAGTCGTCTCTCCG
 57-86/12B6/85b TGTCTCTTCCGTCAGCCTTC [C/T] TCCGCCGCcGTCGTCTCTCCG
 58-86/12B11/85 TCAGGTTTACCTCTATATAT [T/] ATATTTCATGGTATGAAGGT
 30 59-n1/12B11/N2-2 TATCTTGCAAATTGACATT [T/C] CCTTCAGGTTCTAGAAGCTG
 60-85/12C2/86 CGAGAACAGAAGAGAAGAGA [C/] TGGAACACGTCGGACAGTAC
 62-12C11/N2 ACGGGTCCTAGCGCCATGGC [T] ATTTTCTCACC GTTTCTGG
 63-N1/12D10 TTGGGCTTTCCGTTGTTATGA [T] CTTCGTCCTCGTCTATTGCA
 65-85/12F4/86-1 TCCTTGATTCCTTAATAATC [A/T] TTGGCTGGGGGTCTTTCTAA
 35 66-12G5/N1 GCTTGAATAACGATGTCTAC [T] CTGCCTCGGCGTACGGCGGA
 67-85/12G8 CTA AAAAGATCGACGAGTGT [C] CCTTACTACGCTCCATCTAT
 68-12G9/N1-1 AGGTGGGTTTAGCGTGGCAT [C] CGATCCATTGGATGGATCCA
 69-85/12G9/ NGTGGGTTTACCGTATCATT [T] GATCCATTGGATGGATCGAG

70-12B11/N2-1 GCGGATCCTATATTGGGTCT[T]GATGGATTGTTTCTATCCCG
 71-12B11/N2-2 TATCCTGCAAATTGACATT[C]CCTTCAGGTTCTAGAAGCTG
 72-N1/12E10 TACCACGGTCGTACTGGTCG[A]TGTCTGGAACGTACCAAGC
 73-N1/13A3/N2a CTGTCTCagTTTGTGGATC[C/G]AAATCgAATCGAAAGCGTAC
 5 74-N1/13A3/N2b CTGTCTCagTTTGTGGATC[C/G]AAATCaATCGAAAGCGTAC
 75-13E8/N2 ACACTGTTGGAGGACGTGAA[G]AAGATATTCAAGACAACATC
 76-N1/13F6/N2-2 TCTTTTCGTATCTTGCTGAGT[C/T]GTTACGCCTGTCAACACCCG
 77-13F8/N2-1 GGAACCCCTAGGGAGCCACA[G]CTCCTTATGCTAAGCGGCGT
 78-13F8/N2 GATCATAGTATCCGCCGAA[C]CCTAGGGAGCCACAGCTCC
 10 79-85/14B5/86 TTCGGCGGGTCGATCCGGGC[A/G]GAAGACATTGTGAGGTGANN
 80-N1/14C2/N2 GCACCAACATTGTAAACCTA[T/G]AGCTTCTTCCTCAGCCACCT
 81-85/14C2/86-1 GCTGCCACATAGTGAACCTA[T/A]AGCTTCTTCCTCAGCCACCT
 82-N2/14C2/85-2 GCACCAACATTGTGAACCTA[G/A]AGCTTCTTCCTCAGCCACCT
 83-85/14C2/86-2 AGTACATAGCTATTGACTAA[C/G]TTAAGTTCTCTGTATTGTG
 15 84-N2/14C2/85-1 CCTCTATCGCCATGGTTGC[A/T]CCAACATTGTGAACCTAGAG
 85-85/14E2/86-2 TTGACCCCTCGGCAAGCCACC[G/T]GTCAAGCCATGCTGCAGCCT
 86-85/14E2/86-1 AGGCTGCGCTCTCCCAATTC[A/C]AAAGCCAACCTCTAAACCAA
 87-85/14E8/86 AAACATGGAAAGGCTGATA[/G]TCACCGTCAAGCTCACCGTC
 88-85/14E12/86 CAACCTGAAAAATGTTT[A/C/A]CAACGCGCCCGCTTTCTCCA
 20 89-14H10/86 AAGGCCAACAAACGACATTAC[C]TCCATCGTTAGCAACGGAGG
 90-85/14H10/86 TCACCGGCTTGAAGTCTTCC[G/T]CTGCATTCCAGTCACCCGC
 91-85/15A6/86 ACTCAGCTTTCTTATGCCTC[G/]ACTTGCACACACGAATCCA
 92-85/15C4/86 TGCGGCTAACATCTCTGGTG[G/T]TCACCTTAACCCAGCCGTAN
 93-85/15E5/86-1 CGAGGATCACTTCTCTCTGT[G/T]CAAGAAGAAGTTCCGCAAGG
 25 94-N1/15E5/N2-1 CTGTTcCAAGAAGAAGTTCGG[C/T]AAGGTCTACGCTTCCCGCGA
 95-N1/15E5/N2-2 CCCTCTGCTCGTCACGGCGT[T/A]ACGCAGTCTCGGATCTGAC
 96-86/15E5/N2 CCCGCGAGGAGCACGACTAC[A/T]GATTCTCCGTTTTCAAATCC
 97-15E9/86 TCCACTCGCCGGGAAGAAAC[T]CGACAAACCGTTGTCTACTT
 98-N2/15E9 ATGGCTCGCGACGGGTCTCC[G]GTAAACCTCGGAGACAGAT
 30 99-N2/15E9/86 CGGCAGTCTCGAAGCTTCTT[A/]ACTCCACTCGCCGGGAAGAA
 100-85/15E9/86-1 GAATCTAGGAGAGCAGATCT[T/G]CCTCTCTATCTTCAATGTTT
 101-85/15E9/86-2 TCCACTCGCCGGGAAGAAAC[C/T]CGACAAACCGTTGTCTACAT
 102-N1/15E9/N2-1 GTCATGAAGATATTCACTAC[A/G]CCGACTCTCGAAGCTTCTTA
 103-85/15F1/86 GCAGGTAAAATTCTACAGAC[C/A]TTCCCTTTTCATTGTAGTTA
 35 104-85/15F5/86 TCTCCTCCGCCGCGCAAGAA[G/A]AAATCGACAGCGGCGCGTCT
 105-85/15F10/86 GTGCCCTAAAGATACCTCA[A/G]GCTTGGTGTCTGCGCTAATG
 106-N2/15G1 TTCTTCCACAGGTGAAACT[T]GCTAACTTCCCTCCAAGTA
 107-N1/15H7/N2 TATGTATCAGGACAATGTGT[GA/TT]GTGACTGTGGTTGCATCCAT

108-N1/16A1/N2-1 GCTAAGCTACGCAACTGCCA[C/T]CAATCAGGGCAAGCTAAAGG
 109-85/16A5/86 TATACACTCTTTAAAGCGT[G/C]TGTGTGTACCCATCTCTCTT
 110-N1/16B6/N2 ATGGCTGCGTATTGGCTGT[C/T]AAGGCTGGATCTTGGTCCCA
 111-85/16B6/N1 GGATCCATCTCAACTATGGT[A/C]GTATTATCGTTGAGGCTAGG
 5 112-85/16B7/86 GTATGTGATTTCGGAAGAGAA[T/]CAAACCTAAGTGCCGAGAAAG
 113-N1/16D6/N2 GCTAAGGTAGTTGGAGGAGC[CAA/GTG]
 CCACAGCCACGCGACTAAGG
 114-85/16D10/86 CTCACGCTAGCAAGTAATAA[T/G]ATACTGTCTATTTATGGTTA
 115-N1/16E9/N2 AGACTTTCCCCATTCTCTTC[T/A]CCATCCACCGTCGAAACCCA
 10 116-85/16H3/86-1 ACTTCGAAACTGTAAACCTA[A/T]ACTTTAAGAGTTTAGAGCTA
 117-85/16H3/86-2 CACCATCGGAGAAAGAGGTA[C/T]TCGAAACTGTAAACCTAA
 118-85/17A5/86 CTAAGGCGTCTCCTGAAGAA[A/G]TACAGAGAGTCGAAGAAGAT
 119-85/17C7/86 CCGCGGACGACGCTTTCTTC[C/A]TCTGCTCCACCGCGAGCGCC
 120-85/17F7/86 GAGGAGTAGTCTCCATGGCC[G/]AAGAAGAGCGTCGGAGACCTG
 121-85/17G12/86 GAAGTTAGGGCTTCTAAGAT[C/T]AAGTTTCGGCAAGGCTTTAAC
 122-85/18A2/86 TCAAAACTAATATTTCTTTT[G/C]TTGATTGGTAATAAACAGGT
 123-85/18A11/86 TTCCAGTGAAAAGGCATTGT[T/G]CTCCAAATCTCGCTCTGCG
 124-85/18F5/86 AAGCAGCTCTGACTTGAATG[C/A]GAGAGGTTAATCAGACTGTG
 125-85/18H10/86-3 TAGATTGAAGCAATCAAGAA[G/A]ATCTC
 AGACTTCATCAGCCCA
 126-85/19B3/86 GCATCCAACCTCCAAGGATGA[/C]CCTGCCAAGGTGCTGCTAACT
 127-85/19C8/86 GAGCTCAGGGATGGTGGATC[A/T]GACTACCTTGAAAGGGTGT
 128-N1/19F4/N2 TGGGGTTAGTCGAAATAGGT[A/T]AAATGCTTTGAGTATGTGTA
 129-N1/19H1/N2 TACGCGCAGCACGGACTTGC[G/A]ACGCAAGCAATCGAGCTTTT
 25 130-85/20B4/86-1 GAAGCCCATGGTACGGAGCG[G/A]GAGAGAGTCAAGTACTTGGG
 131-N1/20B12/N2 AACGGGTCACTGCTAAATCA[T/A]AAGGATCACAAGGCTGGGAC
 132-85/20C12/86 CTAGCCTACTTTGGGAAAAG[/T]TTCGTTATTGTTTTGTGTGG
 133-85/20D2/86 GACTTCAAGGACTTCGCCGG[A/C]AAATGCTCCGACGCTGTCAA
 134-85/20D3/86-2 GAGGAGGGCTACATGCAGCT[G/A]AAGAGGCTGAGGGGGCTAAA
 30 135-85/20D6/86-4 GATGTTCAACCTATGAAGAA[G/C]AAACACCGAGGACCAACGAG
 136-85/20D6/86-5 CCATTAGTGAGGGAGCATGT[T/A]CCTGTCACATTTGATGATTG
 137-85/20D6/86-8 AAACACATCGCCAAAGATCC[CG/AA]ACAC
 TCGAGAAAAGAGTGGAG
 138-N1/20D8/N2 CTCATAGGCGATCTGGAGTA[T/G]GCAAAATCGAATCTCCTCTCC
 35 139-N1/20E1/N2 TGCACGCCTCACTTGTTCCT[T/A]CCAATCTGACATCAAGGATT
 140-N1/20F1/N2-1 NGTGTTTTTGAGGTGAAAGC[A/T]ACAAATGGAGATACCTTTTT

141-N1/BoC-a2/N3-2 CCCGAGCCATTAGGACAAGA[T/C]GACTT
 GCCGTTTGACCAAAC

142-N1/BOC-A2/N3-1 CCCATCTCATCCTTTCTTGA[A/G]CC
 GTTGAATCAAGCTCCTGG

5 143-N1/BoC-a2/N3-3 TACATTCTCATTGGTTGGTT[C/A]TTG
 GGAATAAAGTACCAAC

144-86/SC3 GCACGCGCTAGAGTTGTTGC[C]AGAAGGAATGAACAATCTGA

145-N3/SC3/N4-1 CTTGAGACCTATAGTCCTGT[A/T]GTTCCGTCCGCCACAGTTCG

146-N3/SC3/N5-1 CACAGTTCGTACAGTTCTTC[A/C]CATTGCCACTGTTATGCACT

10 147-N1/SC3/N3-1 GAAGGCGTCCACTATCTTGA[A/G]ACCTATAGTCCTGTTGTTTCG

148-86/SC3/N4-1 TCCCGGAAATCTTGCTGAAA[A/C]CGTTTACCTGCGACAACCAG

149-B11/N5-1 ATGTCTTCAAAGTGCTCTGT[T]GCAACGCACGTCCGACAACAG

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from a plant being analyzed. Target nucleic acids can be genomic or cDNA. Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202 (each of which is incorporated by reference for all purposes).

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded

DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis depending whether a polymorphism in question has already been characterized. The first type of analysis is sometimes referred to as de novo characterization. This analysis compares target sequences in different individual plants to identify points of variation, i.e., polymorphic sites. The de novo identification of the polymorphisms of the invention is described in the Examples section. The second type of analysis is determining which form(s) of a characterized polymorphism are present in plants under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one member of a species but do not hybridize to the corresponding segment from another member due to the presence of different polymorphic forms in the respective segments from the two members. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15 mer at the 7 position; in a 16 mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect

match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some example of which are described by WO 95/11995 (incorporated by reference in its entirety for all purposes). One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant forms of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (i.e., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers leading to a detectable product signifying the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the

polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer. See, e.g., WO 93/22456.

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)).

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic

mobilities of single-stranded amplification products can be related to base-sequence difference between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in a subject plant at one or more polymorphic sites, this information can be used in a number of methods.

A. Fingerprint Analysis

Analysis of which polymorphisms are present in a plant is useful in determining of which strain the plant is a member an in distinguishing one strain from another. A genetic fingerprint for an individual strain can be made by determining the nucleic acid sequence possessed by that individual strain that corresponds to a region of the genome known to contain polymorphisms. For a discussion of genetic fingerprinting in the animal kingdom, see, for example, Stokening et.al., *Am. J. Hum. Genet.* 48:370-382 (1991). The probability that one or more polymorphisms in an individual strain is the same as that in any other individual strain decreases as the number of polymorphic sites is increased.

The comparison of the nucleic acid sequences from two strains at one or multiple polymorphic sites can also demonstrate common or disparate ancestry. Since the polymorphic sites are within a large region in the genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all the disclosed polymorphic sites) set forth in this application should be inherited without change for at least several generations. Knowledge of plant strain or ancestry is useful, for example, in a plant breeding program or in tracing progeny of a proprietary plant. Fingerprints are also used to identify an individual strain and to distinguish or determine the relatedness of one individual strain to another. Genetic fingerprinting can also be useful in hybrid certification, the certification of seed lots, and the assertion of plant breeders rights under the laws of various countries.

B. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of a plant in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose a plant to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include characteristics such as growth rate, crop yield, crop quality, resistance to pathogens, herbicides, and other toxins, nutrient requirements, resistance to high temperature, freezing, drought, requirements for light and soil type, aesthetics, and height. Other phenotypic traits include susceptibility or resistance to diseases, such as plant cancers. Often polymorphisms occurring within the same gene correlate with the same phenotype.

Correlation is performed for a population of plants, which have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the plants, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a χ -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted.

Correlations between characteristics and phenotype are useful for breeding for desired characteristics. By analogy, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

One can test at least several hundreds of markers simultaneously in order to identify those linked to a gene or chromosomal region. For example, to identify markers linked to a gene conferring disease resistance, a DNA pool is constructed from plants of a segregating population that are resistant and another pool is constructed from plants that are sensitive to the disease. Those two DNA pools are identical except for the DNA sequences at the resistance gene locus and in the surrounding genomic area. Hybridization of such DNA pools to the DNA sequences listed in Table 1 allows the simultaneous testing of several hundreds of loci for polymorphisms. Allelic polymorphism-detecting sequences that

show differences in hybridization patterns between such DNA pools will represent loci linked to the disease resistance gene.

The method just described can also be applied to rapidly identify rare alleles in large populations of plants. For example, nucleic acid pools are constructed from several individuals of a large population. The nucleic acid pools are hybridized to nucleic acids having the polymorphism-detecting sequences listed in Table 1. The detection of a rare hybridization profile will indicate the presence of a rare allele in a specific nucleic acid pool. RNA pools are particularly suited to identify differences in gene expression.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise at least 10 contiguous amino acids of one of the sequences described in Table 1, in any of the allelic forms shown. Some nucleic acid encode full-length proteins.

Genes can be expressed in an expression vector in which a gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a eukaryotic cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene,

both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof, and plant cells. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

The DNA fragments are introduced into cultured plant cells by standard methods including electroporation (From et al., *Proc. Natl Acad. Sci. USA* 82, 5824 (1985), infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., *Molecular Biology of Plant Tumors*, (Academic Press, New York, 1982) pp. 549-560; Howell, US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., *Nature* 327, 70-73 (1987)), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* transformed with a Ti plasmid in which DNA fragments are cloned. The Ti plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and is stably integrated into the plant genome (Horsch et al., *Science*, 233, 496-498 (1984); Fraley et al., *Proc. Natl. Acad. Sci. USA* 80, 4803 (1983)).

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic plants capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Plant regeneration from cultural protoplasts is described in Evans et al., "Protoplasts Isolation and Culture," *Handbook of Plant Cell Cultures* 1, 124-176 (MacMillan Publishing Co., New York, 1983); Davey, "Recent Developments in the Culture and Regeneration of Plant Protoplasts," *Protoplasts*, (1983) - pp. 12-29, (Birkhauser, Basel 1983); Dale, "Protoplast Culture and Plant Regeneration of Cereals and Other Recalcitrant Crops," *Protoplasts* (1983) - pp. 31-41, (Birkhauser, Basel 1983); Binding, "Regeneration of Plants," *Plant Protoplasts*, pp. 21-73, (CRC Press, Boca Raton, 1985). For example, a variant gene responsible for a disease-resistant phenotype can be introduced into the plant to simulate that phenotype. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capeocchi, *Science* 244, 1288-1292 (1989). Such transgenic plants are useful in a variety of screening assays. For example, the transgenic plant can then be treated with compounds of interest and the effect of those compounds on the disease resistance can be monitored. In another example, the transgenic plant can be exposed to a variety of environmental conditions to determine the effect of those conditions on the resistance to the disease.

In addition to substantially full-length polypeptides, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to one allelic gene products but not to a second allelic gene product are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100 or all of the polymorphisms shown in Table 1. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

EXAMPLES

As noted above, the sequences in Table 1 were isolated from *B. napus* and *B. oleracea* using oligonucleotide primers designed from expressed DNA sequences from *Arabidopsis*

thaliana, a relative of *Brassica napus* and member of the *Cruciferae* family. Primers used to amplify *B. napus* and *B. oleracea* alleles were selected for an optimal length of 20 bases \pm 2 based such that their melting temperatures were between 60°C and 65°C. Primers were synthesized on a 20 nmole scale using a high throughput DNA synthesizer capable of producing 96 primers simultaneously in a 96-well format. See Lashkari et al., *Proc. Nat. Acad. Sci.* 92, 7912-7915 (1995). The primers, which have an average length of 21 bases, were positioned within DNA sequences such that PCR products produced with cDNA templates would range between 100 and 450 bp. As introns in *Arabidopsis* genes are of modest size, 60% of the 1,920 primers tested on plant DNA gave PCR products.

The components needed for PCR amplification were mixed in the following proportions for a 96 well microamp tray assembly: 206:1 of 10X PCR reaction buffer, 206:1 of 2 mM dNTPs, 186:1 of 15 mM MgCl₂, 720:1 of sterile ddH₂O and, 20:1 of Taq DNA polymerase (Perkin Elmer). The enzyme was added just prior to dispensing 168:1 of this master mix into 8 tubes. 20:1 of the appropriate forward and reverse primer 10 pmol/l stock solutions was added to each tube. A volume of 14:1 of this mixture was dispensed into each well of the microamp assembly with a BioHit 8-channel pipette. A volume of 5:1 of 20 ng/l template DNA solutions was added to the microamp assembly with a 12-channel pipette. The assembly was centrifuged for 30 sec to ensure that all reagents were mixed. Amplifications were performed in a Perkin Elmer system 9600 thermal cycler with an initial denaturation at 95°C for 1 min followed by 40 cycles of 94°C for 30 sec, 55°C for 30 sec, 72°C for 30 sec and a final extension at 72°C for 5 min. Products were separated by electrophoresis at 120 volts for 1 hr through 2% (w/v) agarose gels prestained with ethidium bromide. The banding patterns of these gels were recorded with an Alpha Innotech gel documentation system.

Any two amplicons obtained from the same primer set with two different plant varieties are said to be homomorphic if they have the same size. A set of 355 homomorphic *Brassica napus* and 250 homomorphic *Brassica oleracea* fragments were

purified with Quiaquick columns and sequenced using dye labeled dideoxy-terminators. See Stryer, *Biochemistry* 2nd. ed., pp. 592-593 (1981). The same primers used for the PCR amplification of the homomorphic DNA fragments were also used for the DNA sequencing of these fragments. The sequences obtained were aligned to identify single nucleotide polymorphisms.

Using VLSIPSTM technology (US 5,143,854; WO 90/15070; WO 92/10092), GeneChipJ was constructed using 20mer-probe sets to identify by hybridization the presence or absence of many of the polymorphisms shown in Table 1 in a sample of plant nucleic acid. The tiling strategy used to create the GeneChipJ is set forth in Figure 1. Tiling strategies can be devised using the guidance provided herein by those skilled in the art. Tiling arrays are described in PCT/US94/12305 (incorporated by reference in its entirety for all purposes). ATiling[®] generally means the synthesis of a defined set of oligonucleotide probes that is made up of a sequence complementary to the sequence to be analyzed (the target sequence), as well as preselected variations of that sequence. The variations usually include substitution at one or more base positions with one or more nucleotides. Tiling strategies are discussed in Published PCT Application No. WO 95/11995 (incorporated by reference in its entirety for all purposes). In general, with a tiled array containing 4L probes one can query every position in a nucleotide containing L number of bases. A 4L tiled array, for example, contains L number of sets of 4 probes, i.e. 4L probes. Each set of 4 probes contains the perfect complement to a portion of the target sequence with a single substitution for each nucleotide at the same position in the probe. See also Chee, M., et. al., *Science*, October, 1996.

The tiling strategy for 20mer probes shown in Figure 1 for a single allele of the polymorphism employed probe sets having a perfect match and a corresponding single-base mismatch at the tenth base in the probe, counting from the 3= end. Each set had 14 pairs of probes that began at 14 successively shifted positions such that the substituted base

lay from 7 bases upstream to 6 bases downstream from the polymorphic site. Two such sets of 28 probes were included to query the polymorphic site for the two alleles, as shown for example, in Figure 1. This collection of 56 probes constituted a detection block. Two such blocks per marker were synthesized to query both the forward and reverse strands. Thus each marker interrogated by the GeneChipJ was represented by a full set of 112 probes.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and individually indicated to be so incorporated by reference. Although the present invention has been described in some detail by way of illustration and example for purposes of clarity and understanding, it will be apparent that certain changes and modifications may be practiced within the scope of the appended claims.